

Human 23565

Carboxypeptidase Activation Peptide Domain

Zinc Carboxypeptidase Domain

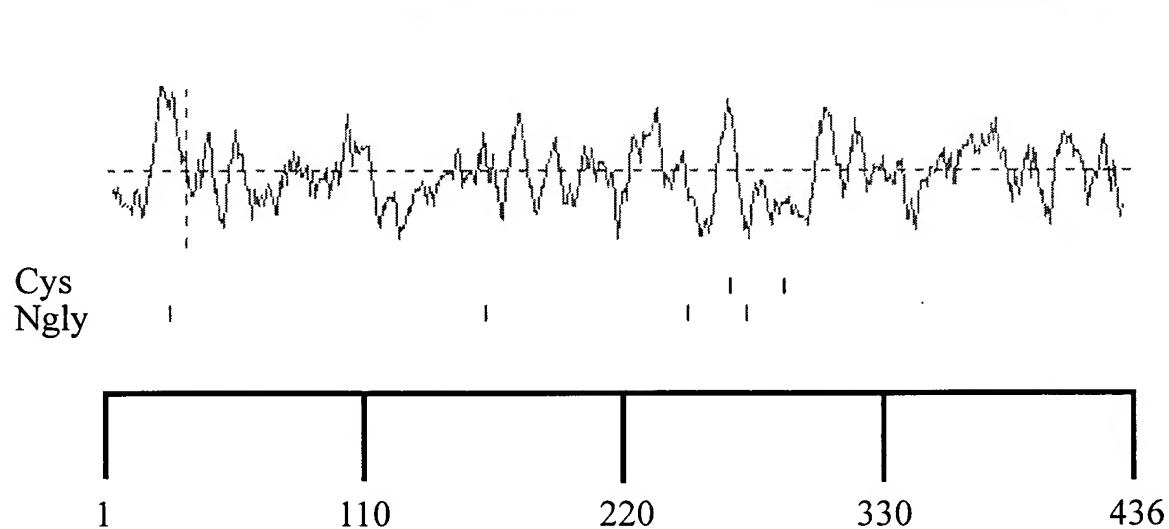


Fig. 1

seqs

Zn_carbOpept: domain 1 of 1, from 139 to 419: score 413.7, E = 1.7e-120

```

*->YhnleeyawldllvsnfPdLvskvsiGksyeGRdlkvLkisdnpat
Yh+leeiy+w+D+ v ++ d+vsk++iG+s++ + vLK+s++
YHTLEEIYSWIDNFMVMEHSDIVSKIQIGNSFENQSILVLFSTG--- 182

Fbh233565f1 139

genePevfavagWiHAREwvtsAtllwllkelvanYgsDktitkllldgld
g++ P+++++g iH+REw+t At w+++++v++Yg D t++l+ +d
GSRHPAIWIDTG-IHSREWITHTATGIWTANKIVSDYGKDRVLTDIILNAMD 231

Fbh233565f1 183

lfyilpvfNpDGyaYsittdsYrMWRKtRspnagsfcvGtDpNRNWyaqw
++i v+NpDG+a++++ + R+WRK+ s ++g fc+G+D+NRNW +++
232 -IFIELVTNPDGFATTHSMN--RLWRKNKSIRPGIFCIGVDLNRNWKSGF 278-

ggmgassysPcSetYeGtapfSepEtkavedfirswlgGGkqnIkayItf
gg g +s +PcSetY+G+ p Se E++a++++fi ++ n ka+I++
279 GGNGSNS-NPCSETYHGSPSPQSESEVAIVNFITAHG-----NFKALISI 322

Fbh233565f1

HsYSqllllyPYgydynlnpdandldelsdlkiaadalsarhgtYytlglp
HsYSq+l+yPYg+ + + ++ +l +l+ k a+ al hg Y g +
323 HSYSQMLMYPYGRLLLEPVSNQRELYDLA--KDAVEALYKVHGIEYIFG-S 369

Fbh233565f1

gsstIYpasAGGsdDwaydvgiikyafteElrpdtdgsyGnPCFl1lpeeql
+s+t+Y+as G + Dwayd g ikyaf fElr dtg YG Fl1P++qI
370 ISTTLYVAS-GITVDWAYDSG-IKYAFSFEFLR-DTGQYG---FLLPATQI 413

Fbh233565f1

iptgsee<-* (SEQ ID NO:4)
ipt++ e
414 IPTAQ-E 419
  
```

Fig. 2A

205120" 363400T

zn_carb: domain 1 of 1, from 139 to 419: score 401.8, E = 6.7e-117

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*->YhsyeeinawlddLarnyPdltsVslisigksyeGRpikvki....
Yh++++ei++w+d+ ++++ d+ Vs i+iG+s+++ i+vlk+++++
YHTLEEEIYSWIDNFMVMEHSDI--VSKIQIGNSFENQSILVLKFstgg 183

..kpavfidagiHAREWiapatalylinqLltneteYskdpdddegsvtkl
++ pa++id giH REWi+ at +++n+++++ Y+kd ++ t++
184 srHPAIWIDTGIHSREWITHTATGIWTANKIVSD---YGKD-RV---LTDI 226

LdkldwyivPvmNPDGYeythtstdrlWRKnRspngasgsqgtwynCyGv
L+ +d++i v+NPDG+++th+ ++rlWRKn s + C+Gv
227 LNAMDIFIELVTNPDGFAFTHS-MNRLWRKNKSIRPG-----IF-CIGV 268

DLNRNfdfhNWgeigGssslpCsetYaGsspfSeWEpEtkaIldfilsne
DLNRN+ ++ +g+ Gs+s+pCsetY+G+sp+S E E+ a+ +fi+ +
269 DLNRNWKSG-FCGN-GSNSNPCSETYHGSPQS--ESEVAAIVNFITAH- 313

igkgrikayislHsysqllyPyGytnatvppngedlhkevakaakaig
g++ka is+Hsysq+l+yPyG + +++n+++l ++ak a+++a+
314 ---GNFKALISIHYSQMLMYPYGRLL-EPVSNQRELY-DLAKDAVEALY 358

dyYfggtlYtpGsssadpdlitlYpasGgsdDwaygtlkgvkysytiEL
+++ G Y G s+++ tly asG++ Dway+ + +ky++ +EL
359 KVH--GIEYIFG-SIST-----TLYVASGITVDWAYDSG--IKYAFSFEL 398

rdtgddagrygFlLppscvkvprmeqiptgeE<-* (SEQ ID NO:5)
rdt g+ygFlLp+ qiipst+ E
399 RDT----GQYGFLLP-----TQIIPTAQE 419
  
```

Fig. 2B

Propep_M14: domain 1 of 1, from 41 to 118: score 100.3, E = 3.8e-26

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*->qVlrvkvadedQvkllkdLentehleLDFWkpdsatpikpgstvDfr
    qVlrv + de+Q++ll dLe ++ DFW++ p++p +vD r
Fbh23565f1 41 QVLRVLAKEKQLSLGLDLEGLKPQKVDFWRG----PARPSLPVDMR 83

    VpaediqavksfLeqsgIhyevlIeDVqelLeeqf<-* (SEQ ID NO:6)
    Vp++++ ++k+ Le++g+ Y+++I D q+lL++
Fbh23565f1 84 VPFSELKDIKAYLESHGLAYSIMIKDIQVLLDEER 118
  
```

Fig. 3